



Matches	87;	Conservative	21;	Mismatches	18;	Indels	4;	Gaps	2;	Db	61	RFSGTGSGTDFETTISLQPEDIATYCOQFDNLPLTFFGGTKVDFK 107
Qy	1	MDFOYQITSFLLTASVILSRGDIQMTQSPSSLASVGDRVTITCSATSSII-TYMSWYQ 58										
Db	1	MDLQVITXFLLSVTYMSRGENVLQTQSPALMAASLGKVMTMSASSVSSSYLHNYQ 60										
Qy	59	QKPGKAPKLLYDTSNLASGVPRFSSGSGTDTYLTITSSLOPEFATYCOQNSYPLT 118										
Db	61	QKSGASPPLIHTSNTLAVGVPARFSSGSGTYSYLTISSEADDTYCOQNSGYP-- 118										
Qy	119	FGGGPKVETK 128										
Db	119	FGSGPKLEIK 128										
RESULT 2												
ID	KV1P_HUMAN	HUMAN	STANDARD;	PRT;	108 AA.							
AC	PO1608											
PP	21-JUL-1986	(Rel. 01, Created)										
DR	21-JUL-1986	(Rel. 01, Last sequence update)										
DR	15-JUL-1999	(Rel. 38, Last annotation update)										
DE	IG KAPPA CHAIN V-I REGION ROY.											
OS	Homo sapiens (Human).											
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.											
OC	NCBI_TaxID=9606;											
OX												
SEQUENCE.												
RP												
MEDLINE	=86174817; PubMed=3083240;											
RA	Dwulet F. E.; O'Connor T. P.; Benson M. D.;											
RA	"Polymorphism in a kappa I primary (Al) amyloid protein (BAN)." Mol. Immunol. 23:73-78(1986).											
RL												
DR	P101878; K1HUBN.											
DR	HSSP; P80362; IWTL.											
DR	InterPro; IPR03006; Ig_MHC.											
DR	InterPro; IPR03596; Ig_Y.											
DR	InterPro; IPR00407; Ig_V.											
DR	SMART; SM00406; IgV; 1.											
DR	Immunoglobulin V region; Amyloid.											
KW												
FT	Immunoglobulin 1	23										
FT	DOMAIN	24										
FT	DOMAIN	34										
FT	DOMAIN	35										
FT	DOMAIN	49										
FT	DOMAIN	50										
FT	DOMAIN	56										
FT	DOMAIN	57										
FT	DOMAIN	88										
FT	DOMAIN	97										
FT	DISULFID	23										
FT	DISULFID	88										
FT	NON_TER	108										
SQ	SEQUENCE	108 AA;	11840 MW;	CD3FD944FB96FD37 CRC64;								
Query Match 67.4%												
Best Local Similarity	78.5%											
Matches	84;	Conservative	11;	Mismatches	11;	Indels	1;	Gaps	1;			
DR	Score 44.15; DB 1; Length 108;											
DR	Best Local Similarity 78.5%; Pred. No. 7.7e-36;											
DR	Matches 84; Conservative 11; Mismatches 11; Indels 1; Gaps 1;											
RESULT 4												
KW	KV10_HUMAN	HUMAN	STANDARD;	PRT;	108 AA.							
FT	KV10_HUMAN											
FT	DOMAIN	24										
FT	DOMAIN	34										
FT	DOMAIN	49										
FT	DOMAIN	56										
FT	DOMAIN	57										
FT	DOMAIN	88										
FT	DOMAIN	97										
FT	DISULFID	23										
FT	DISULFID	88										
FT	NON_TER	108										
SQ	SEQUENCE	108 AA;	11782 MW;	F5ACDE5A313DF3A CRC64;								
Query Match 67.9%												
Best Local Similarity	78.5%											
Matches	84;	Conservative	11;	Mismatches	11;	Indels	1;	Gaps	1;			
DR	Score 44.5%; DB 1; Length 108;											
DR	Best Local Similarity 78.5%; Pred. No. 4e-36;											
DR	Matches 84; Conservative 11; Mismatches 11; Indels 1; Gaps 1;											
RESULT 4												
KW	KV10_HUMAN	HUMAN	STANDARD;	PRT;	108 AA.							
FT	KV10_HUMAN											
FT	DOMAIN	24										
FT	DOMAIN	34										
FT	DOMAIN	49										
FT	DOMAIN	56										
FT	DOMAIN	57										
FT	DOMAIN	88										
FT	DOMAIN	97										
FT	DISULFID	23										
FT	DISULFID	88										
FT	NON_TER	108										
SQ	SEQUENCE	108 AA;	11782 MW;	F5ACDE5A313DF3A CRC64;								
Query Match 67.9%												
Best Local Similarity	78.5%											
Matches	84;	Conservative	11;	Mismatches	11;	Indels	1;	Gaps	1;			
DR	Score 44.5%; DB 1; Length 108;											
DR	Best Local Similarity 78.5%; Pred. No. 4e-36;											
DR	Matches 84; Conservative 11; Mismatches 11; Indels 1; Gaps 1;											
RESULT 4												
KW	KW11_HUMAN	HUMAN	STANDARD;	PRT;	108 AA.							
FT	KW11_HUMAN											
FT	DOMAIN	24										
FT	DOMAIN	34										
FT	DOMAIN	49										
FT	DOMAIN	56										
FT	DOMAIN	57										
FT	DOMAIN	88										
FT	DOMAIN	97										
FT	DISULFID	23										
FT	DISULFID	88										
FT	NON_TER	108										
SQ	SEQUENCE	108 AA;	11782 MW;	F5ACDE5A313DF3A CRC64;								
Query Match 67.9%												
Best Local Similarity	78.5%											
Matches	84;	Conservative	11;	Mismatches	11;	Indels	1;	Gaps	1;			
DR	Score 44.5%; DB 1; Length 108;											
DR	Best Local Similarity 78.5%; Pred. No. 4e-36;											
DR	Matches 84; Conservative 11; Mismatches 11; Indels 1; Gaps 1;											
RESULT 4												
KW	KW12_HUMAN	HUMAN	STANDARD;	PRT;	108 AA.							
FT	KW12_HUMAN											
FT	DOMAIN	24										
FT	DOMAIN	34										
FT	DOMAIN	49										
FT	DOMAIN	56										
FT	DOMAIN	57										
FT	DOMAIN	88										
FT	DOMAIN	97										
FT	DISULFID	23										
FT	DISULFID	88										
FT	NON_TER	108										
SQ	SEQUENCE	108 AA;	11782 MW;	F5ACDE5A313DF3A CRC64;								
Query Match 67.9%												
Best Local Similarity	78.5%											
Matches	84;	Conservative	11;	Mismatches	11;	Indels	1;	Gaps	1;			
DR	Score 44.5%; DB 1; Length 108;											
DR	Best Local Similarity 78.5%; Pred. No. 4e-36;											
DR	Matches 84; Conservative 11; Mismatches 11; Indels 1; Gaps 1;											
RESULT 4												
KW	KW13_HUMAN	HUMAN	STANDARD;	PRT;	108 AA.							
FT	KW13_HUMAN											
FT	DOMAIN	24										
FT	DOMAIN	34										
FT	DOMAIN	49										
FT	DOMAIN	56										
FT	DOMAIN	57										
FT	DOMAIN	88										
FT	DOMAIN	97										
FT	DISULFID	23										
FT	DISULFID	88										
FT	NON_TER	108										
SQ	SEQUENCE	108 AA;	11782 MW;	F5ACDE5A313DF3A CRC6								

RT three-dimensional structure of antibodies, in particular their combining site.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).  
 RN [2]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE=76039568; PubMed=1182131;

RA "The molecular structure of a dimer composed of the variable portions

RT of the Bence-Jones protein RE1 refined at 2.0 Å resolution.";  
 RL Biochemistry 14:1943-1952(1975).  
 CC -1- MISCELLANEOUS : THE C REGION OF THIS CHAIN HAS THE INV (1,2)

CC MARKER.

DR PIR: A01873; KIHORE.

DR InterPro: IPR000006; Ig\_MHC.

DR InterPro: IPR003006; Ig\_V.

DR Pfam: PF00047; Ig\_V.

DR SMART: SM00406; IgV\_1.

DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.

FT DOMAIN 1 23 FRAMEWORK 1.

FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 35 49 FRAMEWORK 2.

FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 57 88 FRAMEWORK 3.

FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.

FT DISULFID 98 107 FRAMEWORK 4.

FT STRAND 23 88

FT STRAND 4 4 FRAMEWORK 1.

FT STRAND 10 10

FT TURN 15 13

FT STRAND 15 16

FT TURN 19 25

FT STRAND 30 31

FT TURN 33 38

FT STRAND 40 41

FT STRAND 45 49

FT STRAND 50 52

FT TURN 53 54

FT TURN 56 57

FT STRAND 60 61

FT TURN 62 67

FT TURN 68 69

FT STRAND 70 75

FT HELIX 80 82

FT STRAND 85 90

FT STRAND 98 98

FT STRAND 102 106

NON\_TER 108 108

SEQUENCE 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match 66.6%; Score 436.5; DB 1; Length 108;

Best Local Similarity 79.2%; Pred. No. 2.3e-5; Indels 1; Gaps 1;

Matches 84; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

Qy 23 DIQMTQSPSSLSASVYGDRTVITCSATSS-TYMSWYQQPGKAPKLLIYDTSNLASGVPS 81

Db 1 DIQMTQSPSSLSASVYGDRTVITCSATSS-TYMSWYQQPGKAPKLLIYDTSNLASGVPS 81

Qy 82 RFSGSGSGTDTLTISSLQPEDFATYYCQWSSYPLTFFGGTRVEIK 127

Db 1 RFSGSGSGAHTFTISSLQPEDIATYYCQYDYLWPWTFQGTRVEIK 107

Qy 82 RFSGSGSGTDTLTISSLQPEDFATYYCQWSSYPLTFFGGTRVEIK 127

Db 61 RFSGSGSGTDTLTISSLQPEDIATYYCQYDYLWPWTFQGTRVEIK 106

Qy 82 RFSGSGSGTDTLTISSLQPEDFATYYCQWSSYPLTFFGGTRVEIK 127

Db 61 RFSGSGSGAHTFTISSLQPEDIATYYCQYDYLWPWTFQGTRVEIK 106

RT OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 RL OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]

RP SEQUENCE.  
 RX MEDLINE=72189444; PubMed=5028201;  
 RA "Rule of antibody structure. The primary structure of a monoclonal  
 RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones  
 protein Au.);  
 RL Koppe-Seyler's 2. Physiol. Chem. 353:345-370(1972).  
 RN [2]

RP X-RAY CRYSTALLOGRAPHY.  
 RX MEDLINE=7702433; PubMed=1234024;  
 RA Behlhammer H.; Schiffer M.; Epp O.; Colman P.M.; Lattman E.E.,  
 RA Schwager P.; Steigemann W.; Schramm H.J.;  
 RT "The structure determination of the variable portion of the  
 RA Bence-Jones protein Au.";  
 RL Biophys. Struct. Mech. 1:139-146(1975).  
 CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY  
 CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V  
 CC REGION OF THE KAPPA CHAIN REL.  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 DR PIR; A01862; KIHOU.  
 DR HSSP; P01607; IREL.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003396; Ig\_V.  
 DR Pfam; PF00047; Ig\_V.  
 DR SMART; SM00406; IgV\_1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FT DISULFID 98 107  
 FT STRAND 108 AA; 11939 MW; E8011187EE6F6FB9 CRC64;  
 Query Match 66.5%; Score 435.5; DB 1; Length 108;  
 Best Local Similarity 79.4%; Pred. No. 2.9e-35; Indels 1; Gaps 1;  
 Matches 85; Conservative 6; Mismatches 1; Indels 1; Gaps 1;  
 Qy 23 DIQMTQSSLSASVYGDRTVITCSATSS-TYMSWYQQPGKAPKLLIYDTSNLASGVPS 81  
 Db 1 DIQMTQSPSSLSASVYGDRTVITCSATSS-TYMSWYQQPGKAPKLLIYDTSNLASGVPS 81  
 Qy 82 RFSGSGSGTDTLTISSLQPEDFATYYCQWSSYPLTFFGGTRVEIK 127  
 Db 61 RFSGSGSGAHTFTISSLQPEDIATYYCQYDYLWPWTFQGTRVEIK 106  
 DE RESULT 6  
 DE KV1\_HUMAN STANDARD; PRT; 108 AA.  
 DE KV1\_HUMAN STANDARD; PRT; 108 AA.  
 AC P80367;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-I REGION WAT.  
 OS Home sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]

RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
 RX MEDLINE=95086080; PubMed=7993911;  
 RA Huang D.-B.; Chang C.-H.; Ainsworth C.; Bruenger A.T.; Schiffer M.,  
 RA Solomon A.; Stevens F.J.; Eulitz M.,

"Comparison of crystal structures of two homologous proteins: structural origin of altered domain interactions in immunoglobulin light-chain dimers." *RT Biochemistry* 33:14848-14857 (1994).

[2] *RT RN SEQUENCE OF 1-35. MEDLINE=8167731; PubMed=6167731; Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M., Popp R.A., Solomon A.; "Characterization and preliminary crystallographic data on the VL-related fragment of the human κ1 Bene Jones Protein Wat." J. Mol. Biol. 147:185-193 (1981).*

COMPLEMENT-DETERMINING 3.  
 DOMAIN 89 97 FRAMEWORK 4.  
 DOMAIN 98 107 BY SIMILARITY.  
 DISULFID 23 88 TN -> SD (IN REF. 2).  
 CONFLICT 30 31  
 NON-TER 108 108 MW: D9941B50FAE697 CRC64;  
 SEQUENCE 108 11737 MW:

Query Match 66.3%; Score 434 5; DB 1; Length 108;  
 Best Local Similarity 77.6%; Pred. No. 3.6e-35; Indels 1; Gaps 1;  
 Matches 83; Conservative 12; Mismatches 11; Indels 1; Gaps 1;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 Homo sapiens (Human). Chordata; Craniata; Vertebrata; Euteleostomi;  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI Tax ID: 9606;

RESULT 7  
V1H\_HUMAN  
CONVENTIONAL  
DRT: 108 AA.

DR	PTR; A01879; KIHUM.	
DR	HSSP; P80362; IWTL.	
DR	InterPro; IPR003006; Ig_MHC.	
DR	InterPro; IPR03596; Ig_v.	
DR	Pfam; PF00047; Ig; 1.	
DR	SMART; SM00406; IgV; 1.	
KW	Immunoglobulin V region.	
FT	DOMAIN 1 23	FRAMEWORK 1.
FT	DOMAIN 24 34	COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN 35 49	COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN 50 56	COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN 57 88	COMPLEMENTARITY-DETERMINING 3.
FT	DOMAIN 69 98	COMPLEMENTARITY-DETERMINING 3.
FT	DOMAIN 99 108	FRAMEWORK 4.
FT	DISULFID 23 88	BY SIMILARITY.
FT	NON_TER 109 109	
SO	SECRETION 109 AA;	11870 MW;
SO		B6ABF4515D55FF5A0 CRC64 ;

Query	Match	Score	DB	Length
Best Local	Similarity	65.8%	1	109
Matches	Conservative	78.7%	No. 8e-35	
23	DIQWQSPSSLASVGDRYTITCSAT-SSITIYMSWYQQPGKAPKLIIYDTNSLASGVPS	11;	Mismatches	10;
v			Indels	2;
			Gaps	2;

Db 1 DVQMTQSPSSLSSAVGDRVLTCRASQSSVDSLWQQKPKAPKLLIEDTSNLQGVPs 60  
 QY 82 RFSSGSGTDTTISQPEFATYCCQONSSYP-LTFFGGTKVEIK 128  
 Db 61 RFSSGSGTDTTISQPEFATYCCQONSSYP-LTFFGGTKVEIK 128  
 QY 61 RFSSGSGTDTTISQPEFATYCCQONSSYP-LTFFGGTKVEIK 128

RESULT 9  
 KV1X\_HUMAN  
 ID KV1X\_HUMAN STANDARD; PRT; 108 AA.  
 AC P04321;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-I REGION DAUDI PRECURSOR.  
 OS Homo sapiens (Human).  
 OC Mammalia; Butheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Homo sapiens (Human).  
 OC Mammalia; Butheria; Chordata; Craniata; Vertebrata; Euteleostomi; Homo sapiens (Human).  
 OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.  
 [1] I.TAXID=9606;

SEQUENCE FROM N.A.  
 MEDLINE=0501448; PubMed=6091049;  
 RA Klobbeck H.G.; Combriato G.; Zachau H.G.;  
 RT Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related.;  
 RL Nucleic Acids Res. 12:6995-7006(1984).

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 CC DR EMBL; X00966; CAA25478-1; ALT\_TERM.  
 DR PIR; A01884; KIHUDI.  
 DR HSSP; P80362; IWTL.  
 DR InterPro; IPR03006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; Igv\_1.  
 DR SMART; SM00406; Igv\_1.  
 KW Immunoglobulin V region; Signal.

FT SIGNAL\_1 1 129 MW; 782B14A649A60E45 CRC64;  
 FT CHAIN 23 129  
 FT DOMAIN 23 45  
 FT DOMAIN 46 56  
 FT DOMAIN 57 71  
 FT DOMAIN 72 78  
 FT DOMAIN 79 110  
 FT DOMAIN 111 119  
 FT DOMAIN 120 129  
 FT DISULFID 45 110  
 FT NON-TER 129 129  
 SQ SEQUENCE 129 AA; CAF076BC7E5574C8 CRC64;

Query Match 65.7%; Score 430.5; DB 1; Length 129;  
 Matches 69.5%;保守性 12; Mismatches 23; Indels 5; Gaps 3;  
 QY 1 MDFOV--QIFSPILLISAVILSRLGDIQMTQSPSSLASAVGDRVLTCSATSSST-YMSWY 57  
 Db 1 MDMRVPAGLGLLWLRV -RCQDQMTQSPSSLASAVGDRVLTICRAGHNTNFSWY 58  
 QY 58 QOKPGKAPKLLIYDTSNLQAGVPSPRFSGSGTYYTLLISSLQPEDFATYCCQWSSYPL 117  
 Db 59 QOKPGKAPKLLIYDTSNLQAGVPSPRFSGSGTYYTLLISSLQPEDFATYCCQWSSYPL 117  
 QY 118 TFGGGTKVEIK 128  
 Db 119 TFGGGTKVEIK 128

Query Match 65.3%; Score 427.5; DB 1; Length 108;  
 Matches 65.3%;保守性 12; Mismatches 11; Indels 1; Gaps 1;  
 QY 23 DIQMTQSPSSLASAVGDRVLTCSATSSST-YMSWYQKPGKAPKLLIYDTSNLASGVPS 81  
 Db 1 DIQMTQSPSSLASAVGDRVLTICRASQDPSHILWQKQSKKAPKLITYSASSLNGVPS 60  
 QY 82 RFSSGSGTDTTISLQPEDFATYCCQONSSYP-LTFFGGTKVEIK 128  
 Db 61 RFSSGSGTDTTISLQPEDFATYCCQONSSYP-LTFFGGTKVEIK 107

RESULT 11  
 KV1W\_HUMAN  
 ID KV1W\_HUMAN STANDARD; PRT; 129 AA.  
 AC P04431;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DE IG KAPPA CHAIN V-I REGION WALKER PRECURSOR.  
 OS Homo sapiens (Human).  
 OC Mammalia; Butheria; Chordata; Craniata; Vertebrata; Euteleostomi; Homo sapiens (Human).  
 OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.  
 QY 119 TFGGGTKVEIK 129

RP SEQUENCE FROM N.A.  
 RX MEDLINE=5014148; PubMed=6091049;  
 RA Klobbeck H.G.; Combriato G.; Zachau H.G.;

RESULT 10  
 KV1S\_HUMAN  
 ID KV1S\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01611;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE IG KAPPA CHAIN V-I REGION WES.  
 OS Homo sapiens (Human).  
 OC Mammalia; Butheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Primates; Catarrhini; Hominidae; Homo.  
 OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.  
 QY 119 TFGGGTKVEIK 129

SEQUENCE FROM N.A.  
 MEDLINE=6778806;  
 RA Kratzin H.; Yang C.; Krusche J.U.; Hilschmann N.;  
 RT "Preparative separation of the tryptic hydrolysate of a protein by  
 monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein  
 Wes)"  
 RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).  
 CC 1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 DR PTR: A01877; KIHUWS: THIS IS A BENCE-JONES PROTEIN.  
 DR HSSP; P80362; IWTL.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; Igv\_1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 107  
 FT DISULFID 23 88  
 FT NON-TER 108 108  
 SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Query Match 65.3%; Score 427.5; DB 1; Length 108;  
 Matches 65.3%;保守性 12; Mismatches 11; Indels 1; Gaps 1;  
 QY 23 DIQMTQSPSSLASAVGDRVLTCSATSSST-YMSWYQKPGKAPKLLIYDTSNLASGVPS 81  
 Db 1 DIQMTQSPSSLASAVGDRVLTICRASQDPSHILWQKQSKKAPKLITYSASSLNGVPS 60  
 QY 82 RFSSGSGTDTTISLQPEDFATYCCQONSSYP-LTFFGGTKVEIK 128  
 Db 61 RFSSGSGTDTTISLQPEDFATYCCQONSSYP-LTFFGGTKVEIK 107

RESULT 11  
 KV1W\_HUMAN  
 ID KV1W\_HUMAN STANDARD; PRT; 129 AA.  
 AC P04431;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DE IG KAPPA CHAIN V-I REGION WALKER PRECURSOR.  
 OS Homo sapiens (Human).  
 OC Mammalia; Butheria; Chordata; Craniata; Vertebrata; Euteleostomi; Homo sapiens (Human).  
 OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.  
 QY 119 TFGGGTKVEIK 129

RP SEQUENCE FROM N.A.  
 RX MEDLINE=5014148; PubMed=6091049;  
 RA Klobbeck H.G.; Combriato G.; Zachau H.G.;

"Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related.";  
Nucleic Acids Res. 12:6995-7006 (1984).

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--> EMBL: X00905; CAA25477.1; ALT_TERM.
  PIR: A01883; KIHUNK.
  HSSP: P01607; JREI.
  InterPro: IPR003006; Ig_MHC.
  InterPro: IPR003596; Ig_V.
  Pfam: PF00047; Ig_1.
  SMART: SM0006; IgV_1.

  Immunoglobulin V region: Signal.

  SIGNAL 1 22  IG KAPPA CHAIN V-I REGION WALKER.
  CHAIN 23 129  FRAMEWORK 1.
  DOMAIN 23 45  COMPLEMENTARITY-DETERMINING 1.
  DOMAIN 46 56  FRAMEWORK 2.
  DOMAIN 57 71  FRAMEWORK 3.
  DOMAIN 72 78  FRAMEWORK 4.
  DOMAIN 79 110  COMPLEMENTARITY-DETERMINING 2.
  DOMAIN 111 119  COMPLEMENTARITY-DETERMINING 3.
  DOMAIN 120 129  FRAMEWORK 5.
  DISULFID 45 110  BY SIMILARITY.
  DISULFID 129 129  NON_TER.
  DISULFID 129 AA; 144069 MR; E941FA07D4AFC2F9 CRC64;
  DISULFID 129 AA; 144069 MR; E941FA07D4AFC2F9 CRC64;

```

UC Eukaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae; Homo  
 OC NCBI\_TaxID=9606;  
 OX [1]  
 RN SEQUENCE  
 RP MEDLINE="71064023; PubMed=5489770;  
 RX Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;  
 RA "The covalent structure of a human gamma G-immunoglobulin. VI. Amino  
 RT acid sequence of the light chain.";  
 RT Biochemistry 9:3155-3161(1970).  
 RL [2]  
 RN DISULFIDE BOND.  
 RP MEDLINE="71064027; PubMed=4923144;  
 RX

FT DOMAIN	50	56	COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN	57	88	FRAMEWORK 3.
FT DOMAIN	89	97	COMPLEMENTARITY-DETERMINING 3.
FT DISULFIDE	98	107	FRAMEWORK 4.
FT NON-TER	23	88	BY SIMILARITY.
SEQUENCE	108 AA;	108 AA;	11834 MW;
			739993A95431434A CRC64;
Query Match	64.5%	Score 422.5;	DB 1; Length 108;
Best Local Similarity	74.8%	Score 422.5;	DB 1; Length 108;
Matches 80;	Conservative 12;	Mismatches 14;	Indels 1;
QY 23 DIQMTQSPSSLSASVGDRVTITCSATSS1-TYMSWYQQPKGAKPLIYDTSNLASGVPS 81			
Db 1 DIQMTQSPSSLSASVGDRVTITCSATSS1-TYMSWYQQPKGAKPLIYDTSNLASGVPS 81			
QY 82 RFSGSGSGTDTYDYLTISSLOPEDFATYYCQWQSSYPLTFFGGTKEIK 128			
Db 1 RFSGSGSGTDTYDYLTISSLOPEDFATYYCQWQSSYPLTFFGGTKEIK 128			
QY 61 RFSGSGSGTDTYDYLTISSLOPEDFATYYCQWQSSYPLTFFGGTKEIK 107			
Db 1 RFSGSGSGTDTYDYLTISSLOPEDFATYYCQWQSSYPLTFFGGTKEIK 107			
RESULT 14			
KV1G_HUMAN			
ID KV1G_HUMAN			STANDARD;
AC P01539;			PRT; 108 AA.
DT 21-JUL-1986			(Rel. 01, Created)
DT 21-JUL-1986			(Rel. 01, Last sequence update)
DT 15-JUL-1999			(Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION GAL.			
OS Homo sapiens (Human).			
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE;			
RX MEDLINE=8327370; PubMed=6410398;			
RA Goni F.; Frangione B.;			
RT "Amino acid sequence of the Fv region of a human monoclonal IgM (protein WE) with antibody activity against 3,4-pyruvylated galactose in Klebsiella polysaccharides K33.";			
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841 (1983).			
CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH WALDENSTROM'S MACROGLOBULINEMIA.			
CC PIR: WALDENSTROM'S MACROGLOBULINEMIA.			
DR PIR: PE01876; K1HUGL.			
DR InterPro: IPR003006; Ig_MHC.			
DR InterPro: IPR003596; Ig_V.			
DR SMART: SM00406; IgV_1.			
DR Immunoglobulin V region; Monoclonal antibody.			
KW FRAMEWORK 1.			
FT DOMAIN 1	23		
FT DOMAIN	24	34	COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN	35	49	FRAMEWORK 2.
FT DOMAIN	50	56	COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN	57	88	FRAMEWORK 3.
FT DOMAIN	89	97	COMPLEMENTARITY-DETERMINING 4.
FT DISULFID	23	88	FRAMEWORK 4.
FT NON-TER	108	108	BY SIMILARITY.
SEQUENCE 108 AA;	11840 MW;	9249B61F0945618C CRC64;	
Query Match	64.4%	Score 421.5;	DB 1; Length 108;
Best Local Similarity	76.6%	Pred. No. 6.4e-14;	
Matches 82;	Conservative 11;	Mismatches 13;	Indels 1;
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Db 1 DIQMTQSPSSLSASVGDRVTITCSATSS1-TYMSWYQQPKGAKPLIYDTSNLASGVPS 81			
QY 82 RFSGSGSGTDTYDYLTISSLOPEDFATYYCQWQSSYPLTFFGGTKEIK 128			
Db 61 RFSGSGSGTDTYDYLTISSLOPEDFATYYCQWQSSYPLTFFGGTKEIK 128			
QY 61 RFSGSGSGTDTYDYLTISSLOPEDFATYYCQWQSSYPLTFFGGTKEIK 107			
Search completed: May 7, 2002, 12:08:53			
Job time: 451 sec			
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Best Local Similarity	78.5%	Pred. No. 6.4e-34;	
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Db 1 DIQMTQSPSSLSASVGDRVTITCSATSS1-TYMSWYQQPKGAKPLIYDTSNLASGVPS 81			
QY 82 RFSGSGSGTDTYDYLTISSLOPEDFATYYCQWQSSYPLTFFGGTKEIK 128			
Db 61 RFSGSGSGTDTYDYLTISSLOPEDFATYYCQWQSSYPLTFFGGTKEIK 128			
QY 82 RFSGSGSGTDTYDYLTISSLOPEDFATYYCQWQSSYPLTFFGGTKEIK 128			

